OIPE

#2

ENTERED

```
 4 <110> APPLICANT: Saba, Julie D.
 5         Fyrst, Henrik
 9 <120> TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
10         POLYNUCLEOTIDES AND MODULATING AGENTS AND
11         METHODS OF USE THEREFOR
13 <130> FILE REFERENCE: 200116.402C2
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/053,510
16 <141> CURRENT FILING DATE: 2002-01-17
18 <160> NUMBER OF SEQ ID NOS: 21
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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23 <211> LENGTH: 1770
24 <212> TYPE: DNA
25 <213> ORGANISM: S. cerevisiae
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28 <221> NAME/KEY: CDS
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34  1               5                  10                  15
36 atg cca att cat tta cta agg gaa gaa ggc gac ttt gcc cag ttt atg    96
37 Met Pro Ile His Leu Leu Arg Glu Glu Gly Asp Phe Ala Gln Phe Met
38                 20                  25                  30
40 att cta acc atc aac gaa tta aaa ata gcc ata cat ggt tac ctc aga   144
41 Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg
42             35                  40                  45
44 aat acc cca tgg tac aac atg ttg aag gat tat ttg ttt gtg atc ttt   192
45 Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe
46         50                  55                  60
48 tgt tac aag cta ata agt aat ttt ttt tat ctg ttg aaa gtt tat ggg   240
49 Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly
50  65                  70                  75                  80
52 ccg gtg agg tta gca gtg aga aca tac gag cat agt tcc aga aga ttg   288
53 Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu
54                 85                  90                  95
56 ttt cgt tgg tta ttg gac tca cca ttt ttg agg ggt acc gta gaa aag   336
57 Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys
58                 100                 105                 110
60 gaa gtc aca aag gtc aaa caa tcg atc gaa gac gaa cta att aga tcg   384
61 Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser
62                 115                 120                 125
64 gac tct cag tta atg aat ttc cca cag ttg cca tcc aat ggg ata cct   432
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RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/053,510   TIME: 12:39:20

Input Set : A:\402c2.app
Output Set: N:\CRF3\02072002\J053510.raw

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65 Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro
66         130                 135                 140
68 cag gat gat gtt att gaa gag cta aat aaa ttg aac gac ttg ata cca     480
69 Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro
70 145                 150                 155                 160
72 cat acc caa tgg aag gaa gga aag gtc tct ggt gcc gtt tac cac ggt     528
73 His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly
74                  165                 170                 175
76 ggt gat gat ttg atc cac tta caa aca atc gca tac gaa aaa tat tgc     576
77 Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys
78             180                 185                 190
80 gtt gcc aat caa tta cat ccc gat gtc ttt cct gcc gta cgt aaa atg     624
81 Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met
82             195                 200                 205
84 gaa tcc gaa gtg gtt tct atg gtt tta aga atg ttt aat gcc cct tct     672
85 Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser
86     210                 215                 220
88 gat aca ggt tgt ggt acc aca act tca ggt ggt aca gaa tcc ttg ctt     720
89 Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu
90 225                 230                 235                 240
92 tta gca tgt ctg agc gct aaa atg tat gcc ctt cat cat cgt gga atc     768
93 Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile
94             245                 250                 255
96 acc gaa cca gaa ata att gct ccc gta act gca cat gct ggg ttt gac     816
97 Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
98             260                 265                 270
100 aaa gct gct tat tac ttt ggc atg aag cta cgc cac gtg gag cta gat    864
101 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
102         275                 280                 285
104 cca acg aca tat caa gtg gac ctg gga aaa gtg aaa aaa ttc atc aat    912
105 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
106     290                 295                 300
108 aag aac aca att tta ctg gtc ggt tcc gct cca aac ttt cct cat ggt    960
109 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
110 305                 310                 315                 320
112 att gcc gat gat att gaa gga ttg ggt aaa ata gca caa aaa tat aaa    1008
113 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
114             325                 330                 335
116 ctt cct tta cac gtc gac agt tgt cta ggt tcc ttt att gtt tca ttt    1056
117 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
118             340                 345                 350
120 atg gaa aag gct ggt tac aaa aat ctg cca tta ctt gac ttt aga gtc    1104
121 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
122         355                 360                 365
124 ccg gga gtc acc tca ata tca tgt gac act cat aaa tat gga ttt gca    1152
125 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
126     370                 375                 380
128 cca aaa ggc tcg tca gtt ata atg tat aga aac agc gac tta cga atg    1200
129 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
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RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/053,510   TIME: 12:39:20

Input Set : A:\402c2.app
Output Set: N:\CRF3\02072002\J053510.raw

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130 385                  390                  395                  400
132 cat cag tat tac gta aat cct gct tgg act ggc ggg tta tat ggc tct    1248
133 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
134                  405                  410                  415
136 cct aca tta gca ggg tcc agg cct ggt gct att gtc gta ggt tgt tgg    1296
137 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
138                  420                  425                  430
140 gcc act atg gtc aac atg ggt gaa aat ggg tac att gag tcg tgc caa    1344
141 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
142          435                  440                  445
144 gaa ata gtc ggt gca gca atg aag ttt aaa aaa tac atc cag gaa aac    1392
145 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
146      450                  455                  460
148 att cca gac ctg aat ata atg ggc aac cct aga tat tca gtc att tca    1440
149 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
150 465                  470                  475                  480
152 ttt tct tca aag acc ttg aac ata cac gaa cta tct gac agg ttg tcc    1488
153 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
154                  485                  490                  495
156 aag aaa ggc tgg cat ttc aat gcc cta caa aag ccg gtt gca cta cac    1536
157 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
158                  500                  505                  510
160 atg gcc ttc acg aga ttg agc gct cat gtt gtg gat gag atc tgc gac    1584
161 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
162          515                  520                  525
164 att tta cgt act acc gtg caa gag ttg aag agc gaa tca aat tct aaa    1632
165 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
166      530                  535                  540
168 cca tcc cca gac gga act agc gct cta tat ggt gtc gcc ggg agc gtt    1680
169 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
170 545                  550                  555                  560
172 aaa act gct ggc gtt gca gac aaa ttg att gtg gga ttc cta gac gca    1728
173 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
174                  565                  570                  575
176 tta tac aag ttg ggt cca gga gag gat acc gcc acc aag tag           1770
177 Leu Tyr Lys Leu Gly Pro Gly Glu Asp Thr Ala Thr Lys . *
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183 <211> LENGTH: 589
184 <212> TYPE: PRT
185 <213> ORGANISM: S. cerevisiae
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191          20                25                30
192 Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg
193      35                40                45
194 Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe
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195      50                      55                      60
196 Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly
197 65                      70                      75                      80
198 Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu
199                 85                      90                      95
200 Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys
201                 100                     105                     110
202 Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser
203         115                     120                     125
204 Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro
205     130                     135                     140
206 Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro
207 145                     150                     155                     160
208 His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly
209                 165                     170                     175
210 Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys
211                 180                     185                     190
212 Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met
213         195                     200                     205
214 Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser
215     210                     215                     220
216 Asp Thr Gly Cys Gly Thr Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu
217 225                     230                     235                     240
218 Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile
219                 245                     250                     255
220 Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
221                 260                     265                     270
222 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
223         275                     280                     285
224 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
225     290                     295                     300
226 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
227 305                     310                     315                     320
228 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
229                 325                     330                     335
230 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
231         340                     345                     350
232 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Leu Asp Phe Arg Val
233         355                     360                     365
234 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
235     370                     375                     380
236 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
237 385                     390                     395                     400
238 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
239                 405                     410                     415
240 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
241         420                     425                     430
242 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
243         435                     440                     445
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Input Set : A:\402c2.app
Output Set: N:\CRF3\02072002\J053510.raw

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244 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
245         450                 455                 460
246 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
247 465                 470                 475                 480
248 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
249                 485                 490                 495
250 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
251             500                 505                 510
252 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
253         515                 520                 525
254 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
255     530                 535                 540
256 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
257 545                 550                 555                 560
258 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
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261         580                 585
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267 <213> ORGANISM: C. elegans
269 <220> FEATURE:
270 <221> NAME/KEY: CDS
271 <222> LOCATION: (1)...(1629)
273 <400> SEQUENCE: 3
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276 1               5                   10                  15
278 ttt gag ctt cga aag ttc aat cca att gtt ctg gtt tct agt act att   96
279 Phe Glu Leu Arg Lys Phe Asn Pro Ile Val Leu Val Ser Ser Thr Ile
280             20                  25                  30
282 gtt gca aca tac gta ctc acc aat ctg aga cat atg cat tta gat gaa  144
283 Val Ala Thr Tyr Val Leu Thr Asn Leu Arg His Met His Leu Asp Glu
284         35                  40                  45
286 atg ggc atc cgg aaa cgt ttg agc act tgg ttt ttc acc act gta aag  192
287 Met Gly Ile Arg Lys Arg Leu Ser Thr Trp Phe Phe Thr Thr Val Lys
288         50                  55                  60
290 cgt gtg cct ttc atc agg aaa atg att gac aaa caa cta aac gaa gta  240
291 Arg Val Pro Phe Ile Arg Lys Met Ile Asp Lys Gln Leu Asn Glu Val
292 65                  70                  75                  80
294 aag gac gag ctt gag aaa agt ctg aga att gtg gat cga agc acc gaa  288
295 Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu
296             85                  90                  95
298 tac ttc act aca atc cca agc cat tca gtt gga aga act gaa gta ctt  336
299 Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu
300             100                 105                 110
302 cgc ctt gct gcc atc tat gat gat ttg gaa gga cca gct ttt ttg gaa  384
303 Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/053,510

DATE: 02/07/2002
TIME: 12:39:21

Input Set : A:\402c2.app
Output Set: N:\CRF3\02072002\J053510.raw

L:15 M:270 C: Current Application Number differs, Wrong Format